

AMSH1	THNEFTTITHVIVP--KQSAGPDYCDMENVEKLFNVQDQHD--LLTIGWIPTQTAFLS
AMSH2	THNEFTTITHVIVP--KQSAGPDYCDMENVEELNVQDQHD--LLTIGWIPTQTAFLS
AMSH	MRNEFTTITHVLIP--KQSAGSDYCTENEEELFLIQDQHQG--LITLGWIPTQTAFLS
Rpn11	TVRVIDVJAMPOS--GIGVSVIAVDPVFQAKMIDMLKQIGRPFMVVGWYHSPGFGCNLS
Jabl	TMIIMDSFLFVIEGTETRVNAQAAAAYTYPAYTENAKQVGRLENAIGWYHSEPGYGCNLS
*****	
AMSH1	SVLHTHCSYQMLPESVAAIVCSPKHKDTG----IIRLTNAGMLIVSACKKKGTH--PH
AMSH2	SVLHTHCSYQMLPESVAAIVCSPKHKDTG----IIRLTNAGMLIVSACKKKGTH--PH
AMSH	SVLHTHCSYQMLPESVAAIVCSPKFQETG----FILTDHGLXKISSCRQKQTH--PH
Rpn11	GVIINTQSFKEALSERAVAVVVDPIQSVKGKVVIDAFLRINAMMIVLGHEFQTTSNLGH
Jabl	GIEVSTQMLNQQFQKPTVAVVIDPTRTISAG---KVNILGAIRTYPKGYKPPDEGPSTYQ
*****	
AMSH1	TKEPRLFSICKHV--LVKDIKI-----IVLDLR
AMSH2	TKEPRLFSIQKFLSGIISGTAL-----EDEPLKIGYGPNGFPLLG1SRS8SPSEQ
AMSH	SKDPPPLFCSCSHVT--VVDRAV-----TITDLR
Rpn11	LNKPSIQALIHGLNRHYYISITINYRKNELEQKMLLNHKKSWMEGTLQDYSEHCKHNE
Jabl	TIPLNKIEDFGVHCKQYYALEVSYFKSSLDRKLLLELLWNKYNVNTLSSSLLTNADYTTG
-----	
AMSH1	L-----
AMSH2	-----
AMSH	-----
Rpn11	-----
Jabl	-----
-----	
AMSH1	-----
AMSH2	-----
AMSH	-----
Rpn11	LDTVVFK-----
Jabl	IKDKLFNQINIS

FIGURE 1

AMSH1	-----MPDHIDVSLSPEERVRALSKLGCNITISEDTPRR	35
AMSH2	MDQPTVNSLKKLAMPDHTDVSLSPEERVRALSKLGCNITISEDTPRR	30
AMSH	-----MSDHWGDVS LPPEDRVRALSQLGSAVEVNEDIPPRR	35
	*****;*****;*****;*****;*****;*****;*****;	
AMSH1	YFRSGVEMERMASVYLEEGNLENAAIVLYNKFITLIVEKLPNHRYDQQCAV	85
AMSH2	YFRSGVEMERMASVYLEEGNLENAAIVLYNKFITLIVEKLPNHRYDQQCAV	100
AMSH	YFRSGVEMERMASVYLEEGNLENAAIVLYNKFITLIVEKLPNHRYDQQCAV	85
	*****;*****;*****;*****;*****;*****;*****;*****;	
AMSH1	PEKQDIMKKLKEIAFPRTDELNDLKKYKVNVEYQEYLQSKNKKYKAEILKK	135
AMSH2	PEKQDIMKKLKEIAFPRTDELNDLKKYKVNVEYQEYLQSKNKKYKAEILKK	150
AMSH	PEKKDITVKKLKEIAFPKAEEIKAELLKRYTKYTYEYNEEKKKEAEELARN	135
	*****;*****;*****;*****;*****;*****;*****;*****;	
AMSH1	LEHQRLIEAERKRIAQMRRQQQLESEQFLIIFEDQLKKQE LARGQ MRSQQTS	185
AMSH2	LEHQRLIEAERKRIAQMRRQQQLESEQFLIIFEDQLKKQE LARGQ MRSQQTS	200
AMSH	MAIQQELEKEKQRVAQQKQQQLEQEQJHAFEMIRNQELEKERIKIVQEF	185
	*****;*****;*****;*****;*****;*****;*****;*****;	
AMSH1	G-LSEQIDGSALS CFS--THQNNSSLNVFADQPNKSDATNYASHSPPVNR	232
AMSH2	G-LSEQIDGSALS CFS--THQNNSSLNVFADQPNKSDATNYASHSPPVNR	247
AMSH	GKVDPLGGPLVPDLEPKPSLDVFPTLTVSSIQPSDCHTTVRPAKPPVVDR	235
	*****;*****;*****;*****;*****;*****;*****;*****;	
AMSH1	ALTPAATLSAVQN LVVEGLRCVVLPEDLCHKFLQLAESNTVRG IETCGIL	282
AMSH2	ALTPAATLSAVQN LVVEGLRCVVLPEDLCHKFLQLAESNTVRG IETCGIL	297
AMSH	SLKPGALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTARGVETCGIL	285
	*****;*****;*****;*****;*****;*****;*****;*****;	
AMSH1	CGKLITNEFTITHVIVPKQSAGPDYCDMENVEELNVQDQHDLITLGLW	332
AMSH2	CGKLITNEFTITHVIVPKQSAGPDYCDMENVEELNVQDQHDLITLGLW	347
AMSH	CGKLITNEFTITHVILPKQSAGSDYCNTNEEE LNLIQDQQGLITLGLW	335
	*****;*****;*****;*****;*****;*****;*****;*****;	
AMSH1	TEPTQTAFLSSV LHTHC SYQLMLPEAI AIVCS PKHHD TGIFR LITNAGML	382
AMSH2	TEPTQTAFLSSV LHTHC SYQLMLPEAI AIVCS PKHHD TGIFR LITNAGML	397
AMSH	TEPTQTAFLSSV LHTHC SYQLMLPEAIVCS PKFQETGFFK LTDHGLE	385
	*****;*****;*****;*****;*****;*****;*****;*****;	
AMSH1	EVSACKKKGJHPHTKEPRLFSTICKHV--LVKDIKIIIVLDLR-----	421
AMSH2	EVSACKKKGJHPHTKEPRLFSTICKFSLSGIISGTALEMPLKIGYGPNGFP	447
AMSH	EISSCRQKGJHPHSKDPPLCSCSHVT--VVDRAVTIDLR-----	424
	*****;*****;*****;*****;*****;*****;*****;*****;	
AMSH1	-----	
AMSH2	LLGISRSSSPSEQQL	461
AMSH	-----	

FIGURE 2

COP9\_su5\_Hs VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG  
COP9\_su5\_Dm VGRMEAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG  
COP9\_su5\_At AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG  
COP9\_su5\_Ce EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG  
AF2198\_Arcfu LPIGMKVFGTVHSHPSPSCRPEEDLSLFRFGKYHIIVCY--PYDENSWKCYNRKGEEV  
PH0451\_Pyrho MPHDESIKGTFHSHPSPFYPSEGDLMFFSKFGGIHIIAAF--PYDEDSVKAFDSEGREV  
TVN1035\_Thevo KPIDFSLVGSVHSHPGVNLPSAADLHFFSKNGLFHLLIAH--PYTMETVAAYTRNGDPV  
MTH971\_Metth LPPFTGAVGGSVHSHPGVNLPSAADLHFFSKNGLFHLLIAH--PYTMETVAAYTRNGDPV  
aq\_1691\_Aquae ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYIIIFSVQ--KGKVASYRSWELKGDKF  
RV1334\_Myctu EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDAHYVLVSTRDPRHELRSYRIVDGAVT  
RadC\_Ecoli IKINASALILAHNHPGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA  
.....HSHP.....S ..D

FIGURE 3

COP9\_su5\_Hs VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTI SAGKVNLG  
COP9\_su5\_Dm VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG  
COP9\_su5\_At AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG  
COP9\_su5\_Ce EGRKEKVVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG  
Pad1\_Dm TGRPEMVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID  
Pad1\_Hs TGRPEMVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID  
Sks1\_Dd TGRDEIVIGWYHSHPGFGCWLSSVDVNTQQSFEQLQSRAVA--VVVDPLQSVRG-KVVID  
Pad1\_Sc TGRDQMVGWYHSHPGFGCWLSSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID  
..... HSHP' ' ' ' ' S ' D

**FIGURE 4**